FIG. 1A

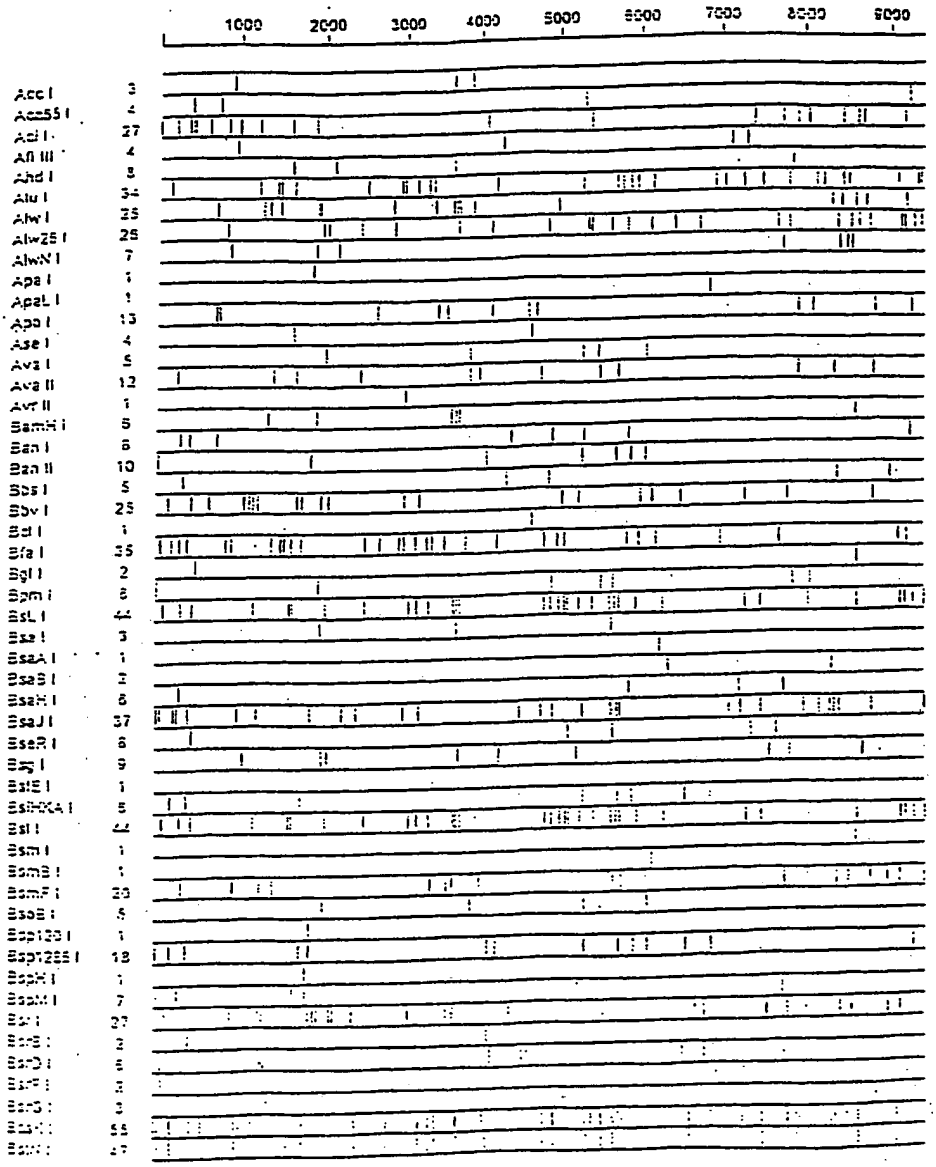

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FIG. 1B

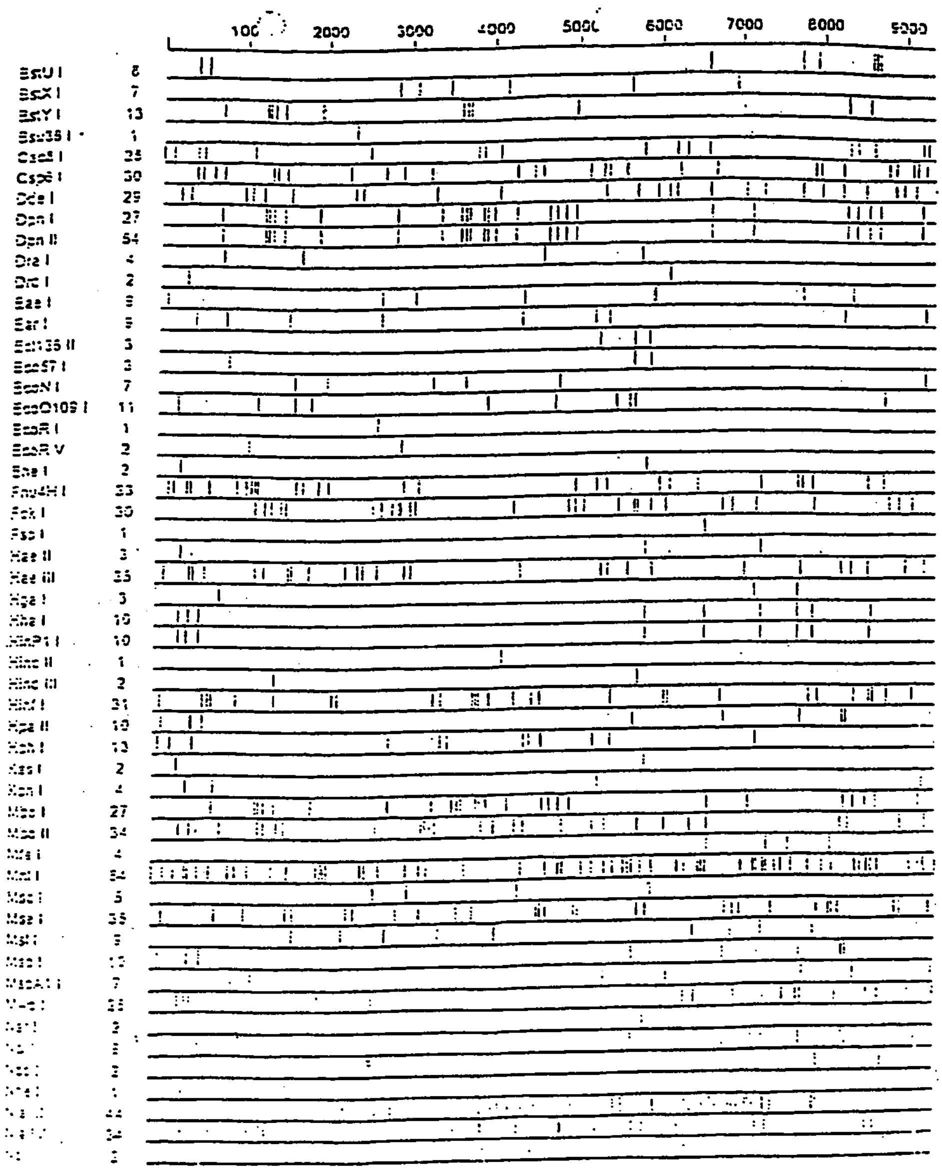

2000
3000
4000
6000
7000
8000
Dpn I 27
Dpn II 54
EcoR I 1
EcoR V 2
Fnu4H I 33
Fok I 30
Hae III 35
Mbo I 27
Mbo II 34

FIG. 1C

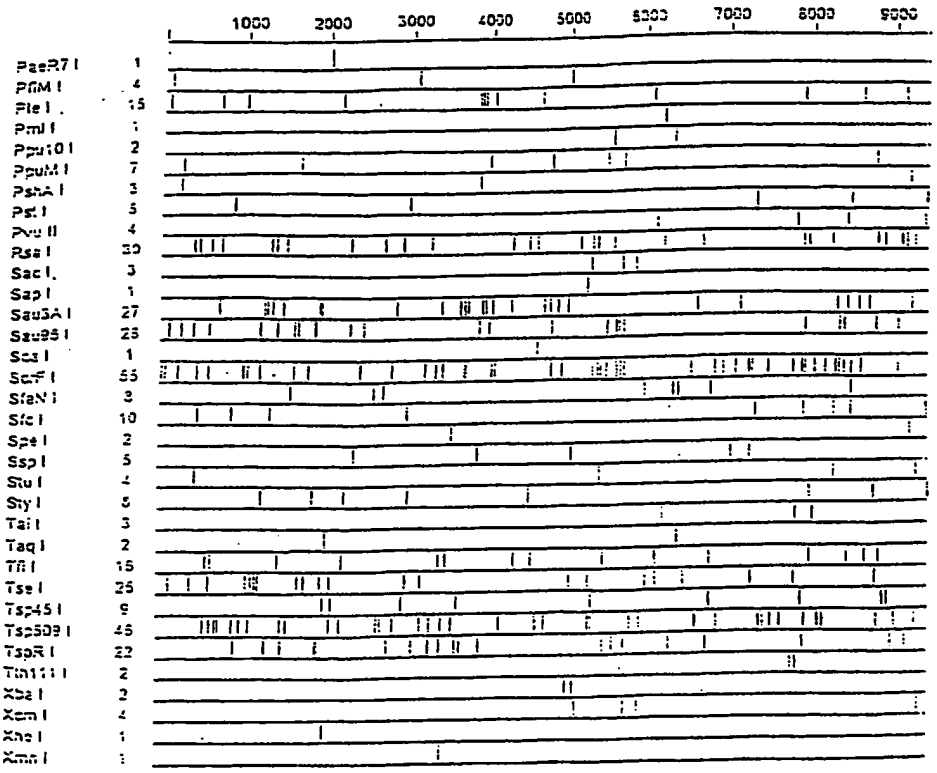

1000
2000
3000
4000
5000
6000
7000
8000
9000
PaeR7 I 1
PflM I 4
Ple I 15
Pml I 1
Ppu10 I 2
PpuM I 7
PshA I 3
Pst I 5
Pvu II 4
Rsa I 30
Sac I 3
Sap I 1
Sau3A I 27
Sau96 I 25
Sca I 1
ScrF I 55
SfaN I 3
Sfc I 10
Spe I 2
Ssp I 5
Stu I 4
Sty I 6
Tai I 3
Taq I 2
Tfi I 15
Tse I 25
Tsp45 I 9
Tsp509 I 45
TspR I 22
Tth111 I 2
Xba I 2
Xcm I 4
Xho I 1
Xmn I 1

FIG. 2

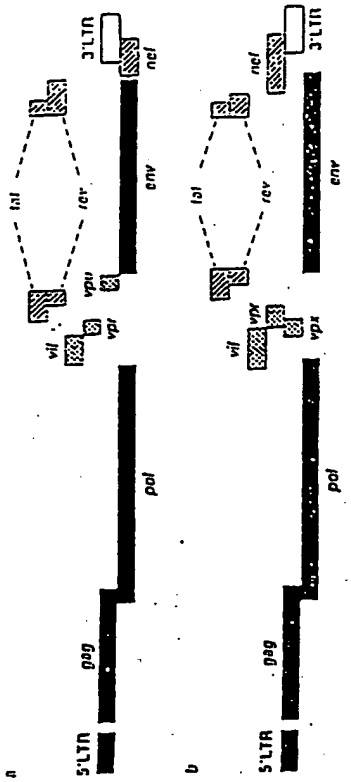

a
5'LTR
gag
pol
vif
vpr
vpu
tat
rev
env
nef
3'LTR
b
5'LTR
gag
pol
vif
vpx
tat
rev
env
nef
3'LTR

FIG. 3A

pROD(PK36) Leader Sequence

```
                    310        320        330        340        350
HIV2ROD     GTTGGCGCCT GAACAGGGAC TTGAAGAAGA CTGAGAAGTC TTGGAACACG
ROD(PK36)   GTTGGCGCCT GAACAGGGAC TTGAAGAAGA CTGAGAAGTC TTGGAACACG

                    360        370        380        390        400
HIV2ROD     GCTGAGTGAA GGCAGTAAGG GCGGCAGGAA CAAACCACGA CGGAGTGCTC
ROD(PK36)   GCTGAGTGAA GGCAGTAAGG GCGGCAGGAA CAAACCACGA CGGAGTGCTC

                    410        420        430        440        450
HIV2ROD     CTAGAAAGGC GCGGGCCGAG GTACCAAAGG CAGCGTGTGG AGCGGGAGGA
ROD(PK36)   CTAGAAAGGC GCGGGCCGAG GTACCAAAGG GAGCGTGTGG AGCGGGAGGA

                    460        470        480        490        500
HIV2ROD     GAAGAGGCCT CCGGGTGAAG GTAAGTACCT ACACCAAAAA CTGTAGCCGA
ROD(PK36)   GAAAGAGGCT CCGGGTGAAG GTAAGTACCT ACACC

                    510        520        530        540        550
HIV2ROD     AAGGGCTTGC TATCCTACCT TTAGACAGGT AGAAGATTGT GGGAGATGGG
ROD(PK36)                                              T GGGAGATGGG
```

FIG. 3B

pROD(SK36) Leader Sequence

```
                    310        320        330        340        350
HIV2ROD     GTTGGCGCCT GAACAGGGAC TTGAAGAAGA CTGAGAAGTC TTGGAACACG
ROD(SK36)   GTTGG

                    360        370        380        390        400
HIV2ROD     GCTGAGTGAA GGCAGTAAGG GCGGCAGGAA CAAACCACGA CGGAGTGCTC
ROD(SK36)

                    410        420        430        440        450
HIV2ROD     CTAGAAAGGC GCGGGCCGAG GTACCAAAGG CAGCGTGTGG AGCGGGAGGA
ROD(SK36)

                    460        470        480        490        500
HIV2ROD     GAAGAGGCCT CCGGGTGAAG GTAAGTACCT ACACCAAAAA CTGTAGCCGA
ROD(SK36)         CT CCGGGTGAAG GTAAGTACCT ACACCAAAAA CTGTAGCCGA

                    510        520        530        540        550
HIV2ROD     AAGGGCTTGC TATCCTACCT TTAGACAGGT AGAAGATTGT GGGAGATGGG
ROD(SK36)   AAGGGCTTGC TATCCTACCT TTAGACAGGT AGAAGATTGT GGGAGATGGG
```

FIG. 3C

pROD(SD36) Leader Sequence

```
                      310        320        330        340        350
HIV2ROD       GTTGGCGCCT GAACAGGGAC TTGAAGAAGA CTGAGAAGTC TTGGAACACG
ROD(SD36)     GTTGG

                      360        370        380        390        400
HIV2ROD       GCTGAGTGAA GGCAGTAAGG GCGGCAGGAA CAAACCACGA CGGAGTGCTC
ROD(SD36)

                      410        420        430        440        450
HIV2ROD       CTAGAAAGGC GCGGGCCGAG GTACCAAAGG CAGCGTGTGG AGCGGGAGGA
ROD(SD36)

                      460        470        480        490        500
HIV2ROD       GAAGAGGCCT CCGGGTGAAG GTAAGTACCT ACACCAAAAA CTGTAGCCGA
ROD(SD36)           CT CCGGGTGAAG GTAAGTACCT ACAC

                      510        520        530        540        550
HIV2ROD       AAGGGCTTGC TATCCTACCT TTAGACAGGT AGAAGATTGT GGGAGATGGG
ROD(SD36)                                               GT GGGAGATGGG
```

FIG. 3D

pROD(CG36) Leader Sequence

```
                      310        320        330        340        350
HIV2ROD       GTTGGCGCCT GAACAGGGAC TTGAAGAAGA CTGAGAAGTC TTGGAACACG
ROD(CG36)     GTTGGCGCCT GAACAGGGAC TTGAAGAAGA CTGAGAAGTC TTGGAACACG

                      360        370        380        390        400
HIV2ROD       GCTGAGTGAA GGCAGTAAGG GCGGCAGGAA CAAACCACGA CGGAGTGCTC
ROD(CG36)     GCTGAGTGAA GGCAGTAAGG

                      410        420        430        440        450
HIV2ROD       CTAGAAAGGC GCGGGCCGAG GTACCAAAGG CAGCGTGTGG AGCGGGAGGA
ROD(CG36)

                      460        470        480        490        500
HIV2ROD       GAAGAGGCCT CCGGGTGAAG GTAAGTACCT ACACCAAAAA CTGTAGCCGA
ROD(CG36)           CT CCGGGTGAAG GTAAGTACCT ACACC

                      510        520        530        540        550
HIV2ROD       AAGGGCTTGC TATCCTACCT TTAGACAGGT AGAAGATTGT GGGAGATGGG
ROD(CG36)                                               GT GGGAGATGGG
```

FIG. 3E

pROD(MR36) Leader Sequence

	310	320	330	340	350
HIV2ROD	GTTGGCGCCT	GAACAGGGAC	TTGAAGAAGA	CTGAGAAGTC	TTGGAACACG
ROD(MR36)	GTTGG				

	360	370	380	390	400
HIV2ROD	GCTGAGTGAA	GGCAGTAAGG	GCGGCAGGAA	CAAACCACGA	CGGAGTGCTC
ROD(MR36)			GCGGCAGGAA	CAAACCACGA	CGGAGTGCTC

	410	420	430	440	450
HIV2ROD	CTAGAAAGGC	GCGGGCCGAG	GTACCAAAGG	CAGCGTGTGG	AGCGGGAGGA
ROD(MR36)	CTAGAAAGGC	GCGGGCCGAG	GTACCAAAGG	GAGCGTGTGG	AGCGGGAGGA

	460	470	480	490	500
HIV2ROD	GAAGAGGCCT	CCGGGTGAAG	GTAAGTACCT	ACACCAAAAA	CTGTAGCCGA
ROD(MR36)	GAAAGAGGCT	CCGGGTGAAG	GTAAGTACCT	ACACC	

	510	520	530	540	550
HIV2ROD	AAGGGCTTGC	TATCCTACCT	TTAGACAGGT	AGAAGATTGT	GGGAGATGGG
ROD(MR36)				GT	GGGAGATGGG

FIG. 4A

HIV-2 pROD(SD36/EM) Sequence of Mutant Region of Envelope
(Insertion mutant)

ROD (6351) ACAGAGGCTT TTGATGCAT
EM ACAGAGGCTT TTGATGCATA GGTAGCGTGA GATCTTAGTG CA

ROD G GAATAATA CA (6380)
EM TAGGTAGC GTGAGATCTT AGTGCAAAGA TCGAATAATA CA.

FIG. 4B pCM-ENV(ROD)(B-14)

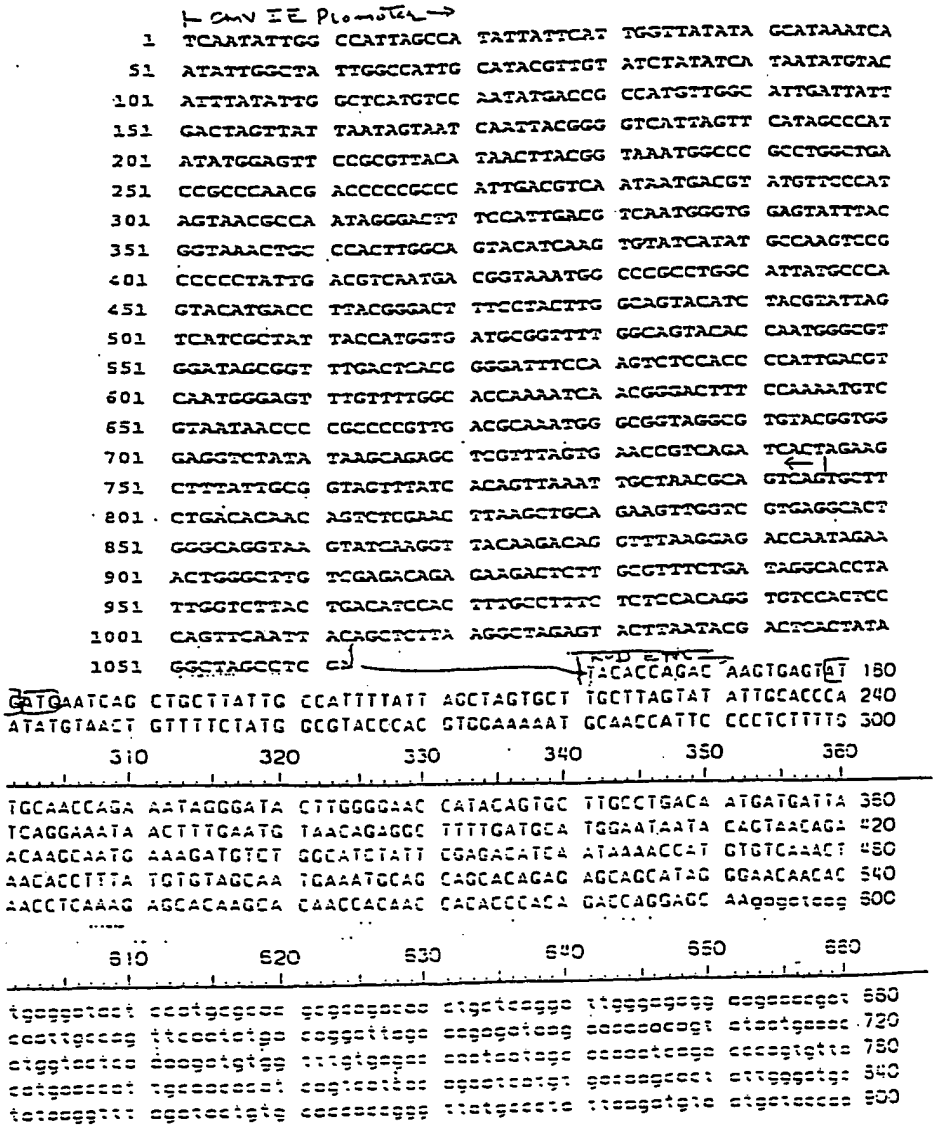


FIG. 4C

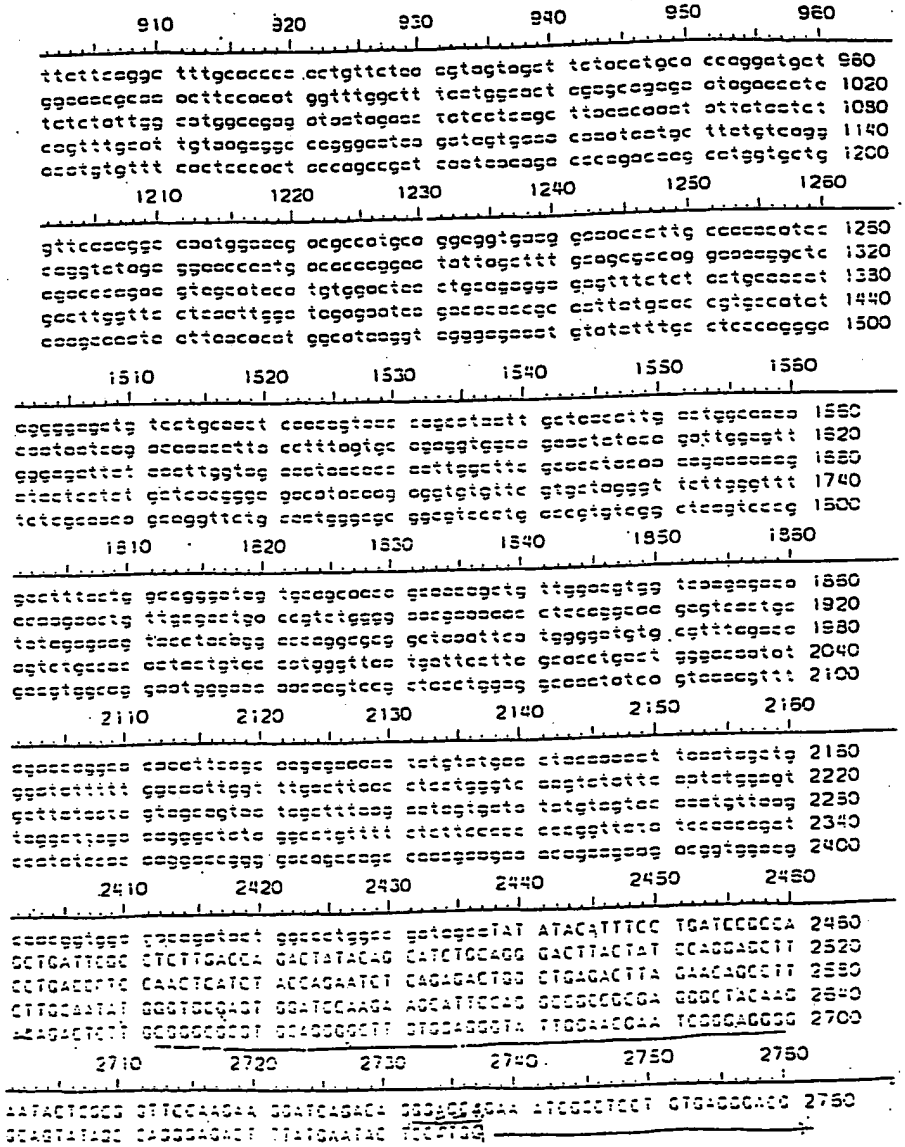

910 920 930 940 950 960
1210 1220 1230 1240 1250 1260
1510 1520 1530 1540 1550 1560
1810 1820 1830 1840 1850 1860
2110 2120 2130 2140 2150 2160
2410 2420 2430 2440 2450 2460
2710 2720 2730 2740 2750 2760

FIG. 4D

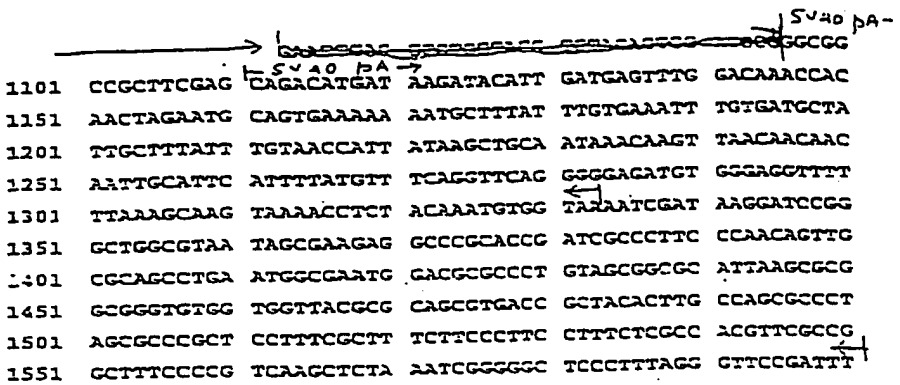

SV40 pA
SV40 pA
1101 CCGCTTCGAG CAGACATGAT AAGATACATT GATGAGTTTG GACAAACCAC
1151 AACTAGAATG CAGTGAAAAA AATGCTTTAT TTGTGAAATT TGTGATGCTA
1201 TTGCTTTATT TGTAACCATT ATAAGCTGCA ATAAACAAGT TAACAACAAC
1251 AATTGCATTC ATTTTATGTT TCAGGTTCAG GGGGAGATGT GGGAGGTTTT
1301 TTAAAGCAAG TAAAACCTCT ACAAATGTGG TAAAATCGAT AAGGATCCGG
1351 GCTGGCGTAA TAGCGAAGAG GCCCGCACCG ATCGCCCTTC CCAACAGTTG
1401 CGCAGCCTGA ATGGCGAATG GACGCGCCCT GTAGCGGCGC ATTAAGCGCG
1451 GCGGGTGTGG TGGTTACGCG CAGCGTGACC GCTACACTTG CCAGCGCCCT
1501 AGCGCCCGCT CCTTTCGCTT TCTTCCCTTC CTTTCTCGCC ACGTTCGCCG
1551 GCTTTCCCCG TCAAGCTCTA AATCGGGGGC TCCCTTTAGG GTTCCGATTT

FIG. 4E HIV-2 Vector System: Native and Pseudotype

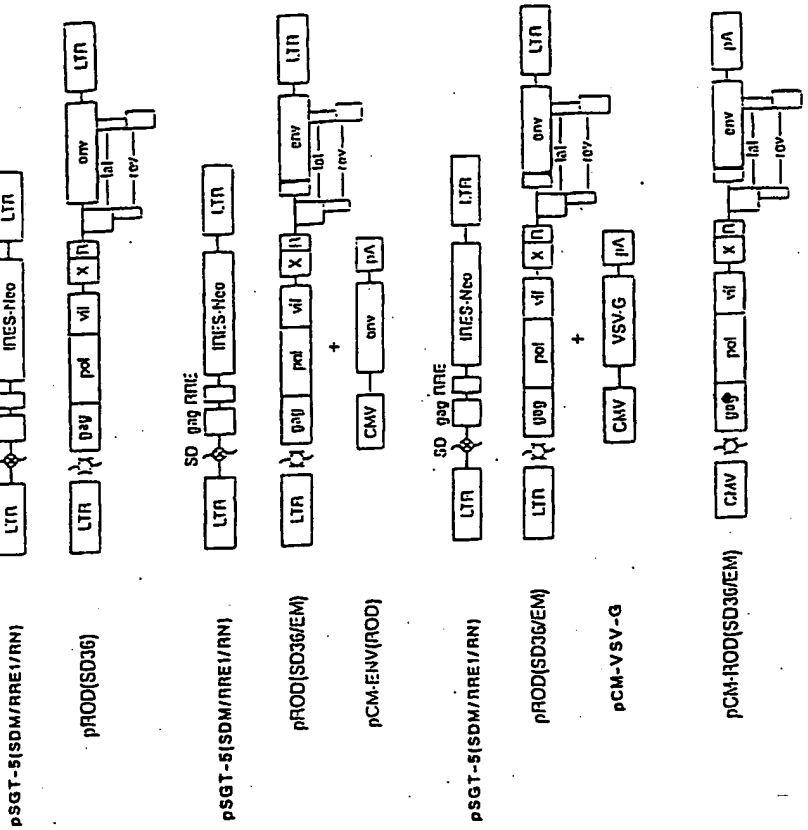


FIG. 5A

SIV 5' LTR Leader Sequence

R—

```
          10                  20                  30                  40                  50
GCTCTGTATT CAGTCGCTCT GCGGAGAGGC TGGCAGATTG AGCCCTGGGA

          60                  70                  80                  90                 100
GGTTCTCTCC AGCACTAGCA GGTAGAGCCT GGGTGTTCCC TGCTAGACTC

         110                 120                 130                 140                 150
TCACCAGCAC TTGGCCGGTG CTGGGCAGAG TGACTCCACG CTTGCTTGCT
                                                    — R |U5—
         160                 170                 180                 190                 200
TAAAGCCCTC TTCAATAAAG CTGCCATTTT AGAAGTAAGC TAGTGTGTGT

         210                 220                 230                 240                 250
TCCCATCTCT CCTAGCCGCC GCCTGGTCAA CTCGGTACTC AATAATAAGA

         260                 270                 280                 290                 300
AGACCCTGGT CTGTTAGGAC CCTTTCTGCT TTGGGAAACC GAAGCAGGAA
         — U5 |Leader—
         310                 320                 330                 340                 350
AATCCCTAGC AGATTGGCGC CTGAACAGGG ACTTGAAGGA GAGTGAGAGA

         360                 370                 380                 390                 400
CTCCTGAGTA CGGCTGAGTG AAGGCAGTAA GGGCGGCAGG AACCAACCAC

         410                 420                 430                 440                 450
GACGGAGTGC TCCTATAAAG GCGCGGGTCG GTACCAGACG GCGTGAGGAG
                                     SD
         460                 470                 480                 490                 500
CGGGAGAGGA AGAGGCCTCC GGTTGCAGGT AAGTGCAACA CAAAAAAGAA

         510                 520                 530                 540                 550
ATAGCTGTCT TTTATCCAGG AAGGGGTAAT AAGATAGAGT GGGAGATGGG

         560
CGTGAGAAAC
```

FIG. 5B

pSIV(SD36)

	320	330	340	350	360
WTL	GATTGGCGC	CTGAACAGGG	ACTTGAAGGA	GAGTGAGAGA	CTCCTGAGTA
SD36	GATTGG				
	370	380	390	400	410
WTL	CGGCTGAGTG	AAGGCAGTAA	GGGCGGCAGG	AACCAACCAC	GACGGAGTGC
SD36					
	420	430	440	450	460
WTL	TCCTATAAAG	GCGCGGGTCG	GTACCAGACG	GCGTGAGGAG	CGGGAGAGGA
SD36					
		SD			
	470	480	490	500	510
WTL	AGAGGCCTCC	GGTTGCAGGT	AAGTGCAACA	CAAAAAAGAA	ATAGCTGTCT
SD36	CTCC	GGTTGCAGGT	AAGTGCAACA	CA	
	520	530	540	550	560
WTL	TTTATCCAGG	AAGGGGTAAT	AAGATAGACT	GGGAG*ATG*GG	CGTGAGAAAC
SD36			GT	GGGAG*ATG*GG	CGTGAGAAAC

FIG. 5C

pSIV(SDM)

	320	330	340	350	360
WTL	GATTGGCGC	CTGAACAGGG	ACTTGAAGGA	GAGTGAGAGA	CTCCTGAGTA
SDM	GATTGGCGC	CTGAACAGGG	ACTTGAAGGA	GAGTGAGAGA	CTCCTGAGTA
	370	380	390	400	410
WTL	CGGCTGAGTG	AAGGCAGTAA	GGGCGGCAGG	AACCAACCAC	GACGGAGTGC
SDM	CGGCTGAGTG	AAGGCAGTAA	GGGCGGCAGG	AACCAACCAC	GACGGAGTGC
	420	430	440	450	460
WTL	TCCTATAAAG	GCGCGGGTCG	GTACCAGACG	GCGTGAGGAG	CGGGAGAGGA
SDM	TCCTATAAAG	GCGCGGGTCG	GTACCAGACG	GCGTGAGGAG	CGGGAGAGGA
		SD			
	470	480	490	500	510
WTL	AGAGGCCTCC	GGTTGCAGGT	AAGTGCAACA	CAAAAAAGAA	ATAGCTGTCT
SDM	AGAGGCCTCC	GGTTG*ATATC*	*G*AGTGCAACA	CAAAAAAGAA	ATAGCTGTCT
	520	530	540	550	560
WTL	TTTATCCAGG	AAGGGGTAAT	AAGATAGAGT	GGGAG*ATG*GG	CGTGAGAAAC
SDM	TTTATCCAGG	AAGGGGTAAT	AAGATAGAGT	GGGAG*ATG*GG	CGTGAGAAAC

FIG. 6A

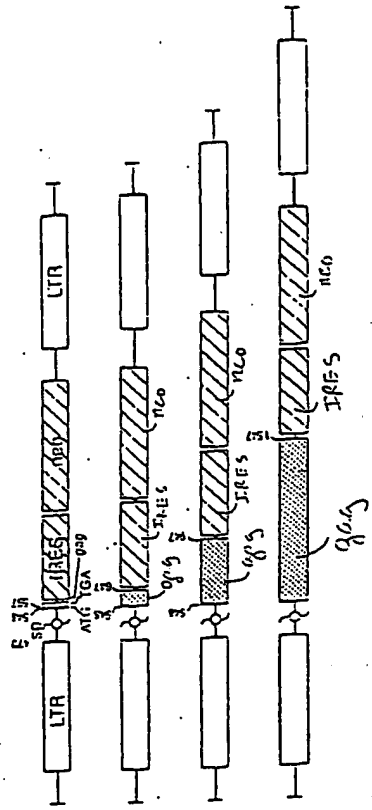

pSGT-3(RN)
pSGT-4(RN)
pSGT-5(RN)
pSGT-6(RN)
LTR
IRES
neo
gag

FIG. 6B

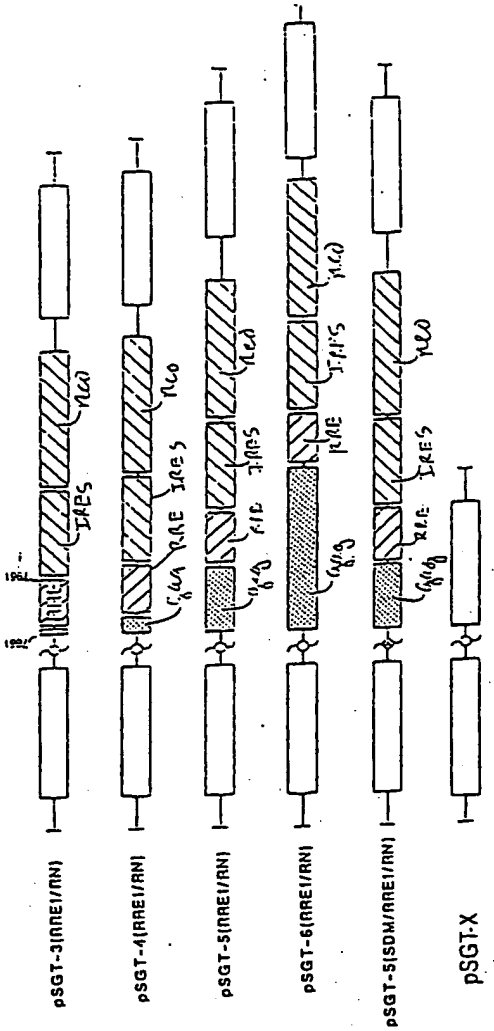

pSGT-3(RRE1/RN)
pSGT-4(RRE1/RN)
pSGT-5(RRE1/RN)
pSGT-6(RRE1/RN)
pSGT-5(SDM/RRE1/RN)
pSGT-X
IRES
neo
RRE

FIG. 7A

```
|U3                530               520
GGAA               GGGCTGTATT        ACAGTGATAG

-530               -520              -510              -500              -490              -480
GAGACGTAGA         GTCCTAGACA        TATACTTAGA        AAAGGAAGAG        GGAATAATTG        GAGACTGGCA

-470               -460              -450              -440              -430              -420
GAACTATACT         CATG GACCAG       GAGTAAGGTA        TCCAAAGTTC        TTTGGGTGGT        TATGGAAGCT

-410               -400              -390              -380              -370              -360
AGTACCAGTA         GATGTCCCAC        AAGA GGGAGA       TGACAGTGAG        ACTCACTGCT        TAGTGCATCC

-350               -340              -330              -320              -310              -300
AGCA CAAACA        AGCAGGTTTG        ATGACCCGCA        TGGAGAAACA        TTAGTTTGGA        GGTTTGACCC

-290               -280              -270              -260              -250              -240
CACGCTAGCT         TTTAGCTACG        AGGCCTTTAT        TCGATACCCA        GAGGAGTTTG        GGTACAAGTC

-230               -220              -210              -200              -190              -180
AGGCCTGCCA         GAGGATGAAT        GGAAGGCAAG        ACTGAAAGCA        AGAGGGATAC        CGTTAGCTA

-170               -160              -150              -140              -130              -120
AAAACAGGAA         CAGCTATACT        TGGTCAGGGC        AGGAAGTAAC        TAACAGAAAA        CAGCTGAGAC

-110               -100              -90               -80               -70               -60
TGCAGGGACT         TTCCAGAAGG        GGCTGTTACC        AGGGGAGGGA        CATGGGAGGA        GCCGGTGGGG

-50                -40               -30               -20               -10               U3|
AACGCCCTCA         TACTTTCTGT        ATAAATGTAC        CCGCTACTCG        CATTGTATTC

|R          10               20                30                40                50                60
GTTCGCTCTG         CGGAGAGGCT        GGCAGATTGA        GCCCTGGGAG        GTTCTCTCCA        GCACTAGCAG

          70               80                90               100               110               120
TGGTCACCTG         GGTGTTCCCT        GCTAGACTCT        CACCAGTGCT        TGGCCGGCAC        TGGGCAGACG

         130               140               150               160               170          R|U5 180
GCTCCACGCT         TGCTTGCTTA        AAAGACCTCT        TAATAAAGCT        GCCAGTTAGA        AGCAAGTTAA

         190               200               210               220               230               240
GTGTGTGCTC         CCATCTCTCC        TAGTCGCCGC        CTGGTCATTC        GGTGTTCATC        TAAAGTAACA

         250               260               270               280               290               300
AGACCCTGGT         CTGTTAGGAC        CCTTTCTGCT        TTGGGAAACC        AAGGCAGGAA        AATCCCTAGC

U5|Leader 310              320               330               340               350               360
AGGTTGGCGC         CCGAACAGGG        ACTTGAAGAA        GACTGAGAAG        CCTTGGAACA        CGGCTGAGTG

         370               380               390               400               410               420
AAGGCAGTAA         GGGCGGCAGG        AACAAACCAC        GACGGAGTGC        TCCTAGAAAA        GCGCAGGCCG
```

FIG. 7B

430	440	450	460	470|—SDM—| 480	
AGGTACCAAG	GGCGGCGTGT	GGAGCGGGAG	TGAAAGAGGC	CTCCGGGTGA	TATCAGTGCC
490	500	510	520	530	540
TACACCAAAT	ACAGTAGCCA	GAAGGGCTTG	TTATCCTACC	TTTAGACGGG	TAGAAGATTG
Leader |gag	560	570	580	590	600
TGGGAGATGC	CATGGTAGGG	CGCGAGAAAC	TCCGTCTTGA	GAGGGAAAAA	AGCAGACGAA
610	620	630	640	650	660
TTAGAAAAGA	TTAGGTTACG	GCCCGGCGGA	AAGAAAAAAT	ATAGGCTAAA	ACATATTGTG
670	680	690	700	710	720
TGGGCAGCGA	ATGAATTGGA	CAGATTCGGA	TTGGCAGAGA	GCCTGTTGGA	GTCAAAAGAG
730	740	750	760	770	780
GGTTGCCAAAA	AAATTCTTAC	AGTTTTAGAT	CCATTAGTAC	CGACAGGGTC	AGAAAATTTA
790	800	810	820	830	840
AAAAGCCTTT	TTAATACTGT	CTGCGTCATT	TGGTGTATAC	ACGCAGAAGA	GAAAGCGAAA
850	860	870	880	890	900
GATACTGAAG	AAGCAAAACA	AAAGGTACAG	AGACATCTAG	TGGCAGAAAC	AAAAACTACA
910	920	930	940	950	gag(955) |poly(L)
GAAAAAATGC	CAAGTACAAG	TAGACCAACA	GCACCACCTA	GCGGGAACGG	AGGAACTCGA
970	980	| RRE(7661) 990	1000	1010	1020
ATGCATGGTG	ACCGCGGCCG	CAGAGGTGTA	TTCGTGCTAG	GGTTCTTAGG	TTTTCTCACA
1030	1040	1050	1060	1070	1080
GCAGGAGCTG	CAATGGGCGC	GGCGTCCTTG	ACGCTGTCGG	CTCAGTCTCG	GACTTTATTG
1090	1100	1110	1120	1130	1140
GCCGGGATAG	TGCAGCAACA	GCAACAGCTG	TTGGACGTGG	TCAAGAGACA	ACAAGAAATG
1150	1160	1170	1180	1190	1200
TTGCGACTGA	CCGTCTGGGG	AACAAAAAAT	CTCCAGGCAA	GAGTCACTGC	TATCGAGAAA
1210	1220	1230	1240	1250	1260
TACTTAAAGG	ACCAGGCGC	AACTAAATTCA	TGGGGATGTG	CGTCTAGACA	AGTCTGCCAC
1270	RRE(7960)| poly(L)	1290	|(8770)	1310	1320
ACTACTGTAC	CATGGGTAGC	GGCCGCTCGC	GAGTAGACCA	TGGAGAGCCC	CAGCAGAAGG
1330	1340	1350	1360	1370	1380
GGAGAAAGGC	TCGTACAAGC	AACAAAATAT	GGATGATGTA	GATTCAGATG	ATGATGACCT
1390	1400	1410	1420	1430	1440
AGTAGGGGTC	CCTGTCACAC	CAAGAGTACC	ATTAAGAGAA	ATGACATATA	GGTTGGCAAG
1450	1460	1470	(8944)| U3 1480	1490	1500
AGAT ATGTCA	CATTTGATAA	AAGAAAAGGG	GGGACTGGAA	GGGCTGTATT	ACAGTGATAG

FIG. 7C

1510	1520	1530	1540	1550	1560
GAGACGTAGA	GTCCTAGACA	TATACTTAGA	AAAGGAAGAG	GGAATAATTG	GAGACTGGCA
1570	1580	1590	1600	1610	1620
GAACTATACT	CATG GACCAG	GAGTAAGGTA	TCCAAAGTTC	TTTGGGTGGT	TATGGAAGCT
1630	1640	1650	1660	1670	1680
AGTACCAGTA	GATGTCCCAC	AAGA GGGAGA	TGACAGTGAG	ACTCACTGCT	TAGTGCATCC
1690	1700	1710	1720	1730	1740
AGCA CAAACA	AGCAGGTTTG	ATGACCCGCA	TGGAGAAACA	TTAGTTTGGA	GGTTTGACCC
1750	1760	1770	1780	1790	1800
CACGCTAGCT	TTTAGCTACG	AGGCCTTTAT	TCGATACCCA	GAGGAGTTTG	GGTACAAGTC
1810	1820	1830	1840	1850	1860
AGGCCTGCCA	GAGGATGAAT	GGAAGGCAAG	ACTGAAAGCA	AGAGGGATAC	CGTTAGCTA
1870	1880	1890	1900	1910	1920
AAAACAGGAA	CAGCTATACT	TGGTCAGGGC	AGGAAGTAAC	TAACAGAAAA	CAGCTGAGAC
1930	1940	1950	1960	1970	1980
TGCAGGGACT	TTCCAGAAGG	GGCTGTTACC	AGGGGAGGGA	CATGGGAGGA	GCCGGTGGGG
1990	2000	2010	2020	U3|R	2040
AACGCCCTCA	TACTTTCTGT	ATAAATGTAC	CCGCTACTCG	CATTGTATTC	AGTCGCTCTG
2050	2060	2070	2080	2090	2100
CGGAGAGGCT	GGCAGATTGA	GCCC TGGGAG	GTTCTCTCCA	GCACTAGCAG	GTAGGCCTG
2110	2120	2130	2140	2150	2160
GGTGTTCCCT	GCTAGACTCT	CACCAGTGCT	TGGCCGGCAC	TGGGCAGACG	GCTCCACGCT
2170	2180	2190	R|		
TGCTTGCTTA	AAAGACCTCT	TAATAAAGC	TGCCA		

FIG. 7D

```
        10         20         30         40         50         60
TCTAGAGGAA TTCCGCCCCT CTCCCTCCCC CCCCCCTAAC GTTACTGGCC GAAGCCGCTT

        70         80         90        100        110        120
GGAATAAGGC CGGTGTGCGT TTGTCTATAT GTTATTTTCC ACCATATTGC CGTCTTTTGG

       130        140        150        160        170        180
CAATGTGAGG GCCCGGAAAC CTGGCCCTGT CTTCTTGACG AGCATTCCTA GGGGTCTTTC

       190        200        210        220        230        240
CCCTCTCGCC AAAGGAATGC AAGGTCTGTT GAATGTCGTG AAGGAAGCAG TTCCTCTGGA

       250        260        270        280        290        300
AGCTTCTTGA AGACAAACAA CGTCTGTAGC GACCCTTTGC AGGCAGCGGA ACCCCCCACC

       310        320        330        340        350        360
TGGCGACAGG TGCCTCTGCG GCCAAAAGCC ACGTGTATAA GATACACCTG CAAAGGCGGC

       370        380        390        400        410        420
ACAACCCCAG TGCCACGTTG TGAGTTGGAT AGTTGTGGAA AGAGTCAAAT GGCTCTCCTC

       430        440        450        460        470        480
AAGCGTATTC AACAAGGGGC TGAAGGATGC CCAGAAGGTA CCCCATTGTA TGGGATCTGA

       490        500        510        520        530        540
TCTGGGGCCT CGGTGCACAT GCTTTACATG TGTTTAGTCG AGGTTAAAAA ACGTCTAGGC

       550        560        570        580        590        600
CCCCCGAACC ACGGGGACGT GGTTTTCCTT TGAAAAACAC GATGATAAGC TTGCCACAAC

       610        620        630        640        650        660
CATGGCTGAA CAAGATGGAT TGCACGCAGG TTCTCCGGCC GCTTGGGTGG AGAGGCTATT

       670        680        690        700        710        720
CGGCTATGAC TGGGCACAAC AGACAATCGG CTGCTCTGAT GCCGCCGTGT TCCGGCTGTC

       730        740        750        760        770        780
AGCGCAGGGG CGCCCGGTTC TTTTTGTCAA GACCGACCTG TCCGGTGCCC TGAATGAACT

       790        800        810        820        830        840
GCAGGACGAG GCAGCGCGGC TATCGTGGCT GGCCACGACG GGCGTTCCTT GCGCAGCTGT

       850        860        870        880        890        900
GCTCGACGTT GTCACTGAAG CGGGAAGGGA CTGGCTGCTA TTGGGCGAAG TGCCGGGGCA

       910        920        930        940        950        960
GGATCTCCTG TCATCTCACC TTGCTCCTGC CGAGAAAGTA TCCATCATGG CTGATGCAAT

       970        980        990       1000       1010       1020
GCGGCGGCTG CATACGCTTG ATCCGGCTAC CTGCCCATTC GACCACCAAG CGAAACATCG

      1030       1040       1050       1060       1070       1080
CATCGAGCGA GCACGTACTC GGATGGAAGC CGGTCTTGTC GATCAGGATG ATCTGGACGA

      1090       1100       1110       1120       1130       1140
AGAGCATCAG GGGCTCGCGC CAGCCGAACT GTTCGCCAGG CTCAAGGCGC GCATGCCCGA

      1150       1160       1170       1180       1190       1200
CGGCGAGGAT CTCGTCGTGA CCCATGGCGA TGCCTGCTTG CCGAATATCA TGGTGGAAAA

      1210       1220       1230       1240       1250       1260
TGGCCGCTTT TCTGGATTCA TCGACTGTGG CCGGCTGGGT GTGGCGGACC GCTATCAGGA

      1270       1280       1290       1300       1310       1320
CATAGCGTTG GCTACCCGTG ATATTGCTGA AGAGCTTGGC GGCGAATGGG CTGACCGCTT

      1330       1340       1350       1360       1370       1380
CCTCGTGCTT TACGGTATCG CCGCTCCCGA TTCGCAGCGC ATCGCCTTCT ATCGCCTTCT

      1390       1400       1410
TGACGAGTTC TTCTGAGCGG GATCGGCTAC C
```

FIG. 7E

pSGT-5(SDM) 5'LTR-Leader Sequence

	10	20	30	40	50
HIV2ST	GTTCGCTCTG	CGGAGAGGCT	GGCAGATTGA	GCCCTGGGAG	GTTCTCTCCA
pSGT5(SDM)	GTTCGCTCTG	CGGAGAGGCT	GGCAGATTGA	GCCCTGGGAG	GTTCTCTCCA
	60	70	80	90	100
HIV2ST	GCACTAGCAG	TGGTCACCTG	GGTGTTCCCT	GCTAGACTCT	CACCAGTGCT
pSGT5(SDM)	GCACTAGCAG	TGGTCACCTG	GGTGTTCCCT	GCTAGACTCT	CACCAGTGCT
	110	120	130	140	150
HIV2ST	TGGCCGGCAC	TGGGCAGACG	GCTCCACGCT	TGCTTGCTTA	AAAGACCTCT
pSGT5(SDM)	TGGGCGGCAC	TGGGCAGACG	GCTCCACGCT	TGCTTGCTTA	AAAGACCTCT
	160	170	180	190	200
HIV2ST	TAATAAAGCT	GCCAGTTAGA	AGCAAGTTAA	GTGTGTGCTC	CCATCTCTCC
pSGT5(SDM)	TAATAAAGCT	GCCAGTTAGA	AGCAAGTTAA	GTGTGTGCTC	CCATCTCTCC
	210	220	230	240	250
HIV2ST	TAGTCGCCGC	CTGGTCATTC	GGTGTTCATC	TAAAGTAACA	AGACCCTGGT
pSGT5(SDM)	TAGTCGCCGC	CTGGTCATTC	GGTGTTCATC	TAAAGTAACA	AGACCCTGGT
	260	270	280	290	300
HIV2ST	CTGTTAGGAC	CCTTTCTGCT	TTGGGAAACC	AAGGCAGGAA	AATCCCTAGC
pSGT5(SDM)	CTGTTAGGAC	CCTTTCTGCT	TTGGGAAACC	AAGGCAGGAA	AATCCCTAGC
	310	320	330	340	350
HIV2ST	AGGTTGGCGC	CCGAACAGGG	ACTTGAAGAA	GACTGAGAAG	CCTTGGAACA
pSGT5(SDM)	AGGTTGGCGC	CCGAACAGGG	ACTTGAAGAA	GACTGAGAAG	CCTTGGAACA
	360	370	380	390	400
HIV2ST	CGGCTGAGTG	AAGGCAGTAA	GGGCGGCAGG	AACAAACCAC	GACGGAGTGC
pSGT5(SDM)	CGGCTGAGTG	AAGGCAGTAA	GGGCGGCAGG	AACAAACCAC	GACGGAGTGC
	410	420	430	440	450
HIV2ST	TCCTAGAAAA	GCGCAGGCCG	AGGTACCAAG	GGCGGCGTGT	GGAGCGGGAG
pSGT5(SDM)	TCCTAGAAAA	GCGCAGGCCG	AGGTACCAAG	GGCGGCGTGT	GGAGCGGGAG
	460	470	480	490	500
HIV2ST	TGAAAGAGGC	CTCCGGGTGA	AGGTAAGTGC	CTACACCAAA	TACAGTAGCC
pSGT5(SDM)	TGAAAGAGGC	CTCCGGGTGA	TATCAGTGC	CTACACCAAA	TACAGTAGCC
	510	520	530	540	550
HIV2ST	AGAAGGGCTT	GTTATCCTAC	CTTTAGACGG	GTAGAAGATT	GTGGGAGATG
pSGT5(SDM)	AGAAGGGCTT	GTTATCCTAC	CTTTAGACGG	GTAGAAGATT	GTGG AGATG

FIG. 7F

pSGT-5(SDM) Leader Sequence

	310	320	330	340	350
HIV2ST	AGGTTGGCGC	CCGAACAGGG	ACTTGAAGAA	GACTGAGAAG	CCTTGGAACA
pSGT5(SDM)	AGGTTGGCGC	CCGAACAGGG	ACTTGAAGAA	GACTGAGAAG	CCTTGGAACA

	360	370	380	390	400
HIV2ST	CGGCTGAGTG	AAGGCAGTAA	GGGCGGCAGG	AACAAACCAC	GACGGAGTGC
pSGT5(SDM)	CGGCTGAGTG	AAGGCAGTAA	GGGCGGCAGG	AACAAACCAC	GACGGAGTGC

	410	420	430	440	450
HIV2ST	TCCTAGAAAA	GCGCAGGCCG	AGGTACCAAG	GGCGGCGTGT	GGAGCGGGAG
pSGT5(SDM)	TCCTAGAAAA	GCGCAGGCCG	AGGTACCAAG	GGCGGCGTGT	GGAGCGGGAG

		SD			
	460	470	480	490	500
HIV2ST	TGAAAGAGGC	CTCCGGGTGA	*AGGTA*AGTGC	CTACACCAAA	TACAGTAGCC
pSGT5(SDM)	TGAAAGAGGC	CTCCGGGTGA	*TATC*AGTGC	CTACACCAAA	TACAGTAGCC

	510	520	530	540	550
HIV2ST	AGAAGGGCTT	GTTATCCTAC	CTTTAGACGG	GTAGAAGATT	GTGGGAGATG
pSGT5(SDM)	AGAAGGGCTT	GTTATCCTAC	CTTTAGACGG	GTAGAAGATT	GTGG AGATG

FIG. 7G

pSGT-5(SDX) Leader Sequence

	310	320	330	340	350
HIV2ST	AGGTTGGCGC	CCGAACAGGG	ACTTGAAGAA	GACTGAGAAG	CCTTGGAACA
pSGT5(SDX)	AGGTTGGCGC	CCGAACAGGG	ACTTGAAGAA	GACTGAGAAG	CCTTGGAACA

	360	370	380	390	400
HIV2ST	CGGCTGAGTG	AAGGCAGTAA	GGGCGGCAGG	AACAAACCAC	GACGGAGTGC
pSGT5(SDX)	CGGCTGAGTG	AAGGCAGTAA	GGGCGGCAGG	AACAAACCAC	GACGGAGTGC

	410	420	430	440	450
HIV2ST	TCCTAGAAAA	GCGCAGGCCG	AGGTACCAAG	GGCGGCGTGT	GGAGCGGGAG
pSGT5(SDX)	TCCTAGAAAA	GCGCAGGCCG	AGGTACCAAG	GGCGGCGTGT	GGAGCGGGAG

		SD			
	460	470	480	490	500
HIV2ST	TGAAAGAGGC	CTCCGGGTGA	AGGTAAGTGC	CTACACCAAA	TACAGTAGCC
pSGT5(SDX)	TGAAAGAGGC	CTCCGG	GC	CTACACCAAA	TACAGTAGCC

	510	520	530	540	550
HIV2ST	AGAAGGGCTT	GTTATCCTAC	CTTTAGACGG	GTAGAAGATT	GTGGGAGATG
pSGT5(SDX)	AGAAGGGCTT	GTTATCCTAC	CTTTAGACGG	GTAGAAGATT	GTGG AGATG

FIG. 8

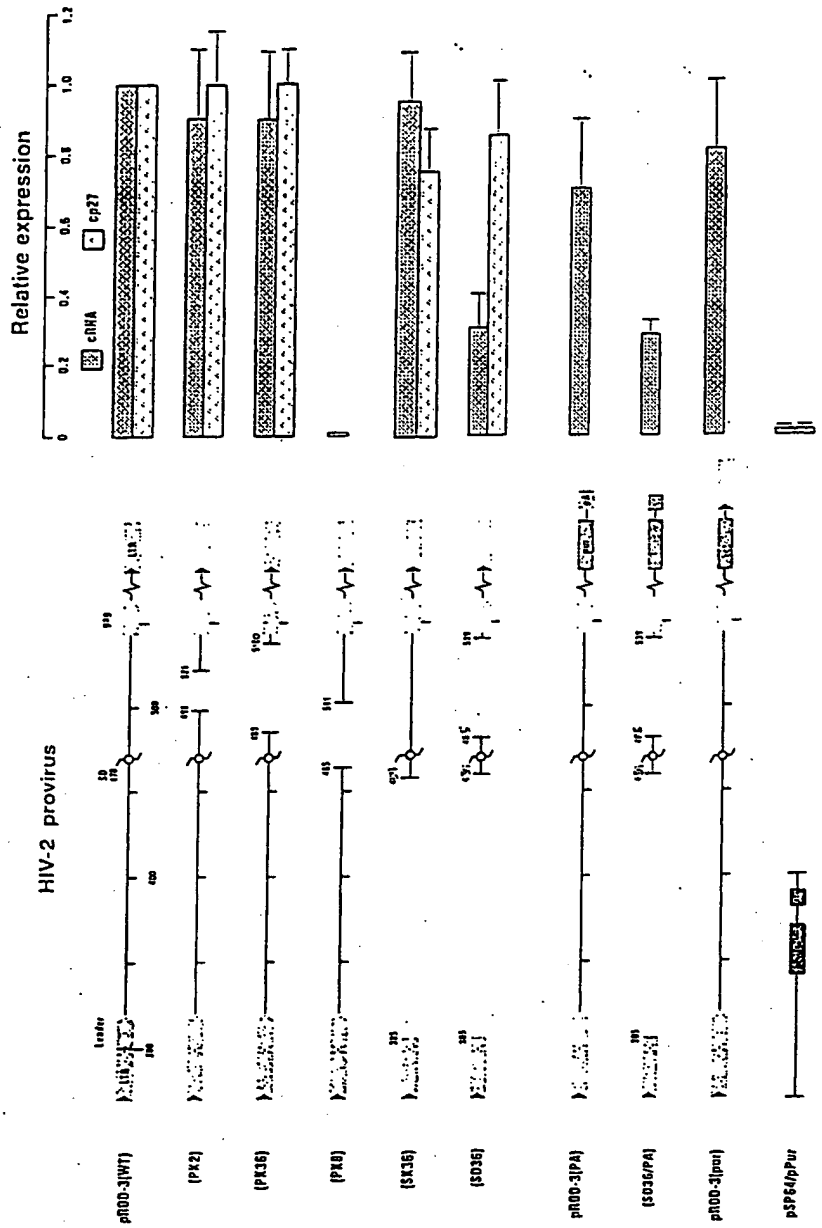

Relative expression
cRNA
cp27
HIV-2 provirus
pROD-3(WT)
(PX2)
(PX35)
(PX8)
(SX35)
(SD35)
pROD-3(PA)
(SD35/PA)
pROD-3(pol)
pSP64/pPur

FIG. 9

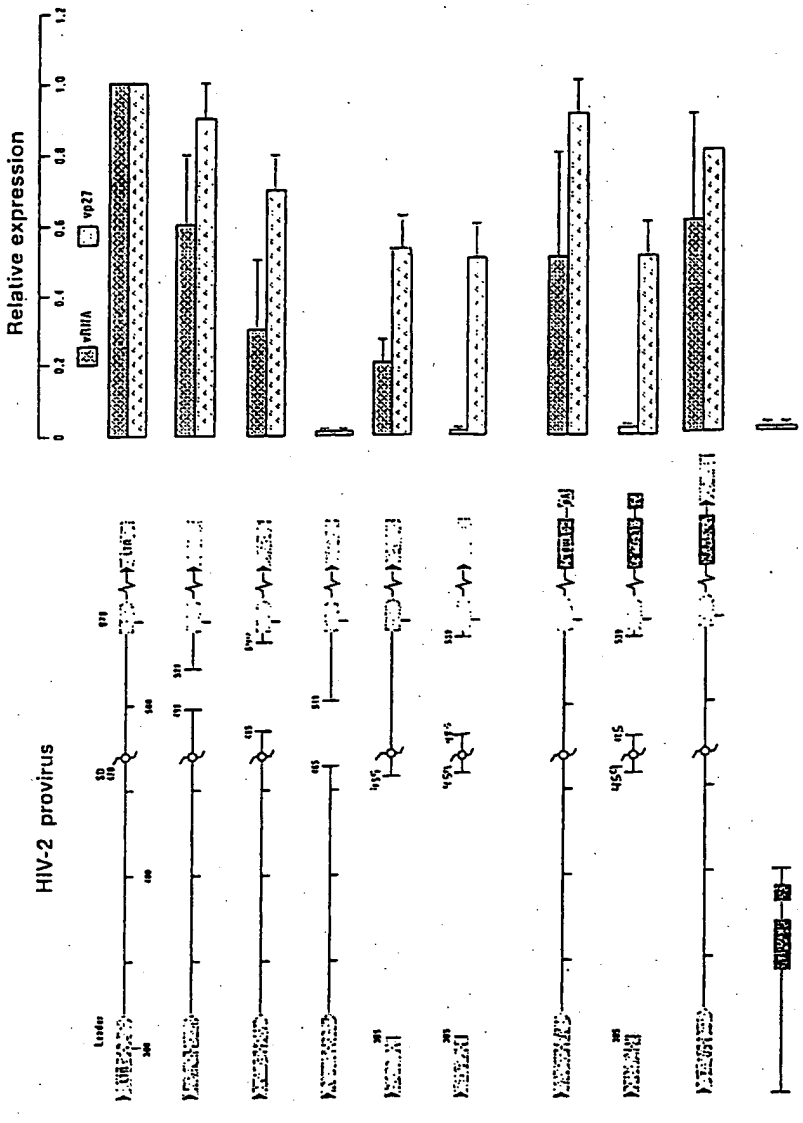

Relative expression
0
0.2
0.4
0.6
0.8
1.0
vpIIIA
vp27
HIV-2 provirus
pROD-3(WT)
(PK2)
(PK36)
(PK8)
(SK36)
(SD36)
pROD-3(PA)
(SD36/PA)
pROD-3(pur)
pSP64/pPur

FIG. 10

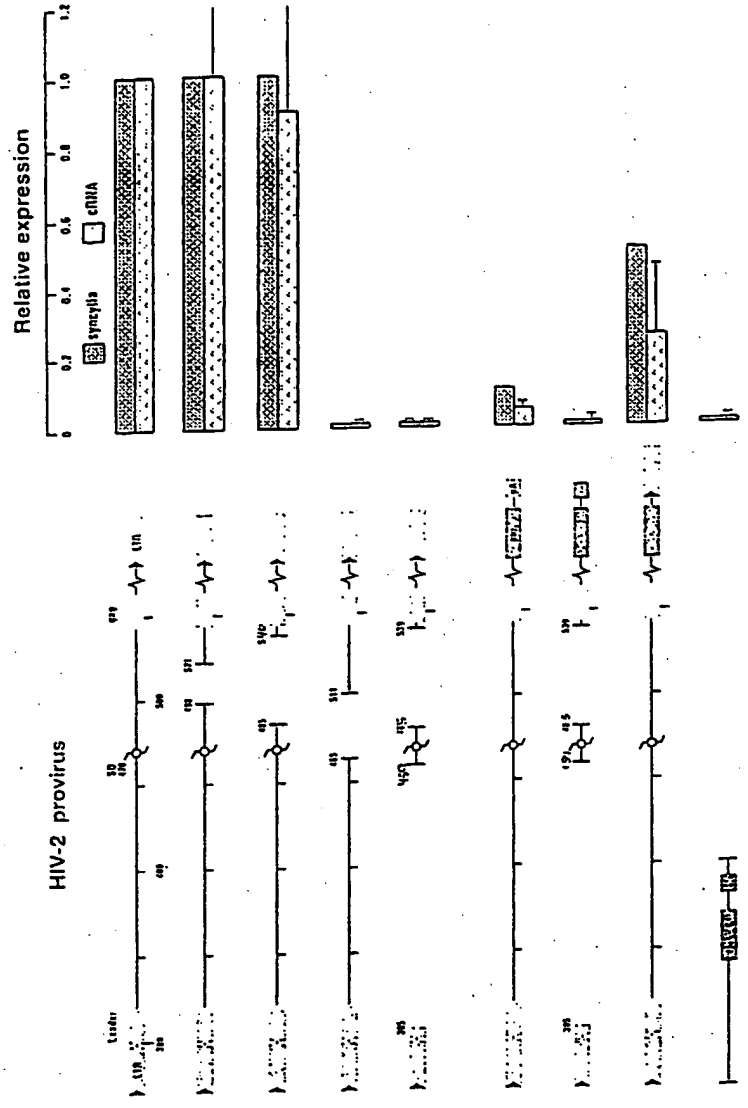
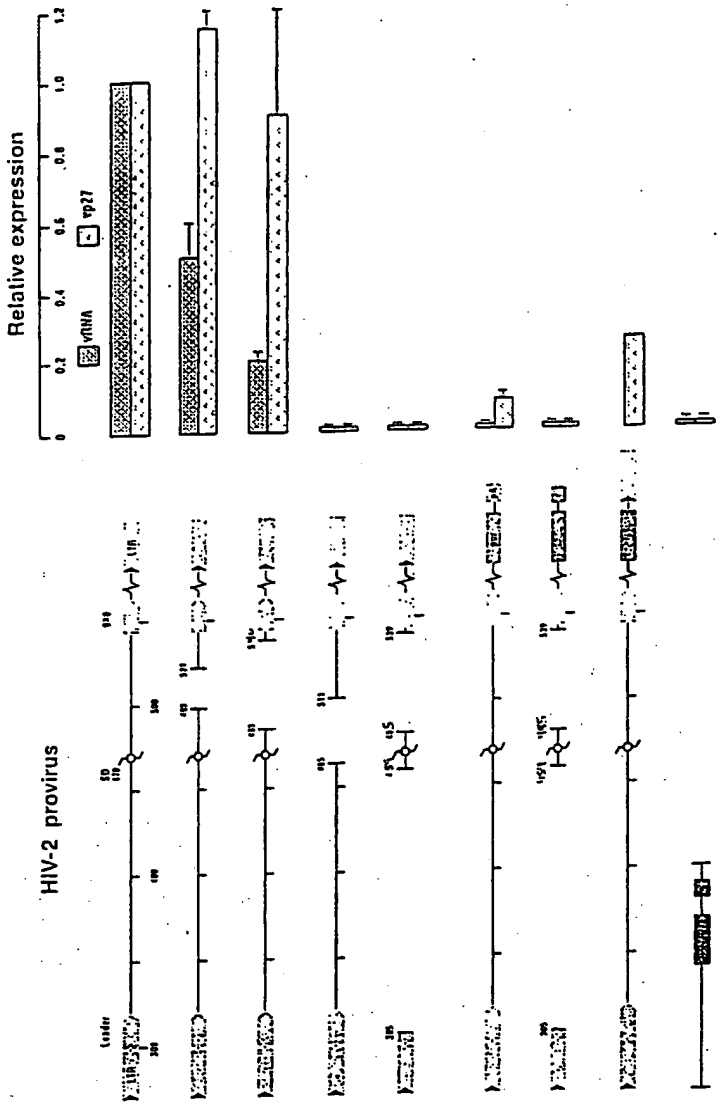

Relative expression
syncytia
cDNA
HIV-2 provirus
pROD-3(WT)
(PK2)
(PK35)
(PK6)
(SD36)
pROD-3(PA)
(SD36/PA)
pROD-3(pur)
pSP64/pPur

FIG. 11


Relative expression
vRNA
vp27
HIV-2 provirus
pROD-3(WT)
(PK2)
(PK35)
(PK8)
(SD35)
pROD-3(PA)
(SD38/PA)
pROD-3(pur)
pSP64/pPur

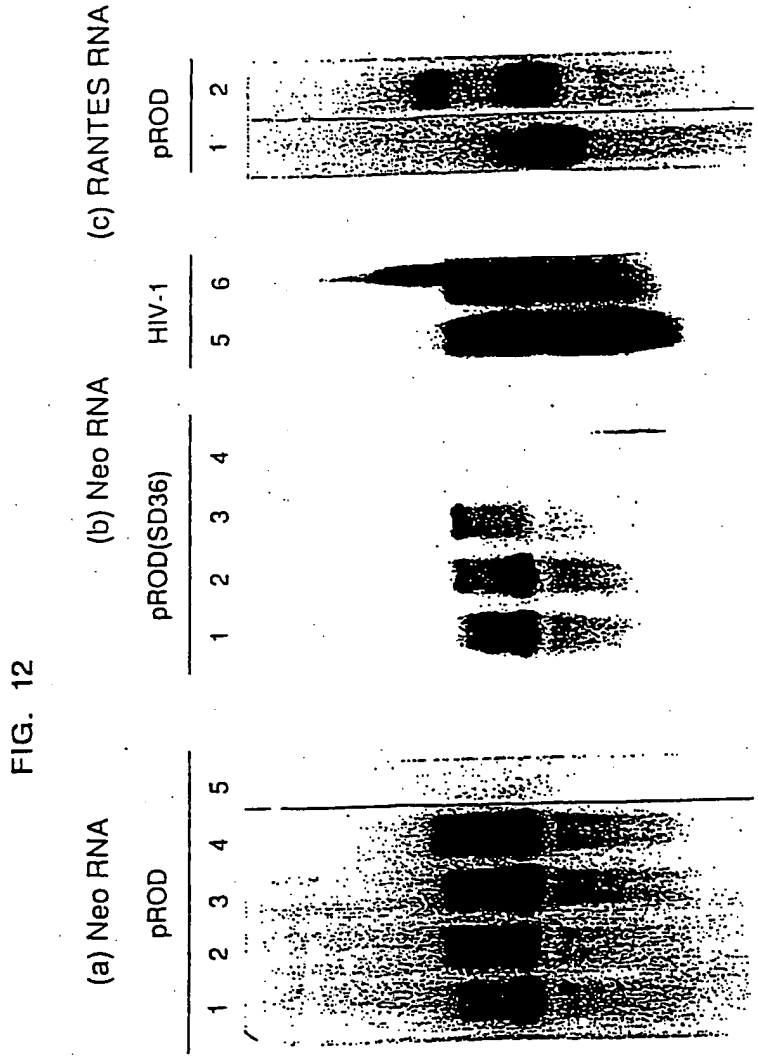
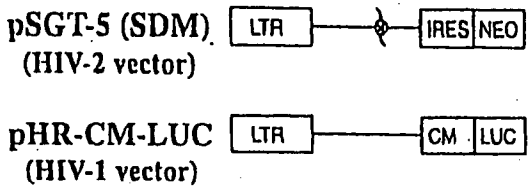

(a) Neo RNA
pROD
1 2 3 4 5
(b) Neo RNA
pROD(SD36)
1 2 3 4
HIV-1
5 6
(c) RANTES RNA
pROD
1 2

FIG. 12

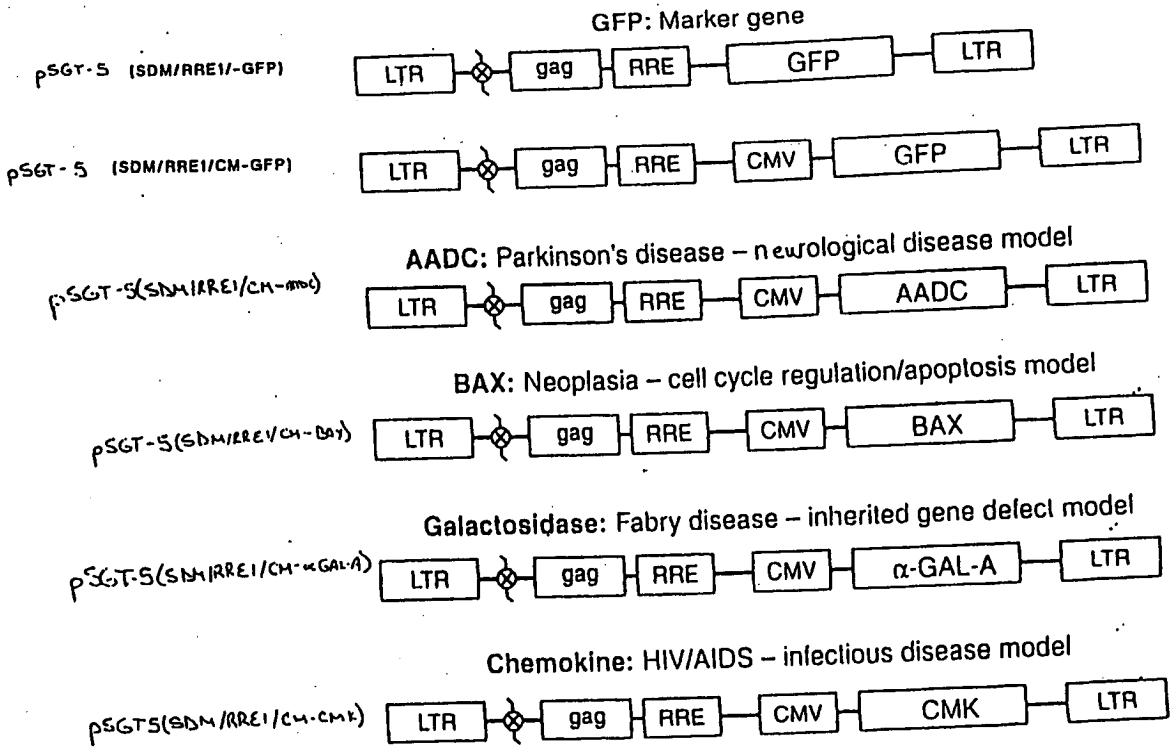
FIG. 13



	% Vector RNA packaged	
	HIV-2 system pROD(SD36)	HIV-1/VSV system
pSGT-5 (SDM) (HIV-2 vector)	8.3 ± 1.2	9.9 ± 0.8
pHR-CM-LUC (HIV-1 vector)	1.0 ± 0.2	16.3 ± 6.5

FIG. 14

HIV-2 Lentivirus Vectors: Gene Transfer Models



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